

OIPE

RAW SEQUENCE LISTING

DATE: 12/20/2001

PATENT APPLICATION: US/10/010,065

TIME: 21:04:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\12202001\J010065.raw

```

4 <110> APPLICANT: Allen, Keith D.
5     Matthews, William
6     Moore, Mark
8 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
9     RECEPTOR GENE DISRUPTIONS
12 <130> FILE REFERENCE: R-648
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/010,065
C--> 15 <141> CURRENT FILING DATE: 2001-12-05
17 <150> PRIOR APPLICATION NUMBER: US 60/251,804
18 <151> PRIOR FILING DATE: 2000-12-06
20 <150> PRIOR APPLICATION NUMBER: US 60/266,044
21 <151> PRIOR FILING DATE: 2001-02-01
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1944
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
32 <400> SEQUENCE: 1
33 caggggtctcc cttgcaacct gaggagaggt gcacacactc tgaggaccta ggtgtgcaac 60
34 ctctgccaga tgtggggcgt ggctaccagc aggcattgcc ctcaccacag tccactgtcc 120
35 ccacctgctg ctgctgctgt tgggtgctgc atgtctgcca gaggcaccct ctgccaggt 180
36 aatggacttt ttgtttgaga agtggagct ctatagtac caatgtcacc acaacctaa 240
37 cctgctgccc ccacctactg agctggctct taacagaacc ttcgacaact actcctgctg 300
38 gcctgacacc cctcccaaca ccactgccaa catttcctgc ccctggtacc taccttgggtg 360
39 ccacaaagtg cagcaccgcc tagtggtcaa gaggtgtggg cccgatggg agtgggttcg 420
40 agggccacgg gggcagccgt ggcgcaacgc ctcccaatgt cagttggatg atgaagagat 480
41 cgagggtccag aaggggggtg ccaagatgta tagcagccag caggtgatgt acaccgtggg 540
42 ctacagtctg tccctggggg ccttgctcct tgcgctggtc atcctgctgg gcctcaggaa 600
43 gctgcaactg acccgaaaact acatccatgg gaacctgttt gcgtcctttg tgctcaaggc 660
44 tggctctgtg ttggtcatcg attggctgct gaagacacgg tacagccaga agattggcga 720
45 tgacctcagt gtgagcgtct ggctcagtga cggggcgatg gccggctgca gagtggccac 780
46 agtgatcatg cagtacggca tcatacccaa ctattgctgg ttgctggtag agggcgtgta 840
47 cctgtacacg ctgctgagcc ttgccacct ctctgagagg agcttctttt ccctctacct 900
48 gggcattggc tgggggtgcg ccctgctgtt tgtcatcccc tgggtggtgg tcaagtgtct 960
49 gtttgagaat gttcagtgtt ggaccagcaa tgacaacatg ggattctggt ggatcctgct 1020
50 tattcctgtc ttcctggcct tactgatcaa ttttttcac tttgtccaca tcattcaact 1080
51 tcttgtggcc aagctgcgtg cccatcagat gcactatgct gattacaagt tccggctggc 1140
52 caggtccacg ctgaccctca tccctctgct ggggggtccac gaggtggtct ttgcctttgt 1200
53 gactgacgag catgcccagg gcaccctgcg ctccaccaag ctcttttttg acctgttcc 1260
54 cagctccttc caggggtctg tgggtggctgt tctctactgt ttcctcaaca aggaggtgca 1320
55 ggcagagctg atgcggcggt ggaggcaatg gcaagaaggc aaagctcttc aggaggaaa 1380
56 gttggccagc agccatggca gccacatggc ccagcaggg ccttgctcat gtgatccctg 1440
57 tgagaaactt cagcttatga gtgcaggcag cagcagtggt actggctgtg tgccctctat 1500
58 ggagacctcg ctggccagta gtctcccaag gttggtgac agccccacct gaatctccac 1560
59 ttggagccta ggcaggttgt gttcaagaaa gggcctcaga ggacaaccca gagccagatg 1620
60 cccggccaag gttgaagagc caaagcagca agacagcagc ttgtactgtg cacactcccc 1680

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61 taacctgtcc tagcctggca caggccacag tgacagagta ggggttggat atgatggaga 1740
62 agccatgtta tctatgaact ctgagtgttc ccatgtgtgt tgacatggtc cctgtaccca 1800
63 gatatgtcct tcagtaaaaa gctcgagtgg agctgctgca cagctcgtgg acagcaggct 1860
64 tgaagcccc agggacgggg tttgggaggg cggggatgag cagcacactc agcaggtgga 1920
65 gcgctagtgc aaccaggaa agaa 1944
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 485
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus musculus
72 <400> SEQUENCE: 2
73 Met Pro Leu Thr Gln Leu His Cys Pro His Leu Leu Leu Leu Leu Leu
74 1 5 10 15
75 Val Leu Ser Cys Leu Pro Glu Ala Pro Ser Ala Gln Val Met Asp Phe
76 20 25 30
77 Leu Phe Glu Lys Trp Lys Leu Tyr Ser Asp Gln Cys His His Asn Leu
78 35 40 45
79 Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp
80 50 55 60
81 Asn Tyr Ser Cys Trp Pro Asp Thr Pro Pro Asn Thr Thr Ala Asn Ile
82 65 70 75 80
83 Ser Cys Pro Trp Tyr Leu Pro Trp Cys His Lys Val Gln His Arg Leu
84 85 90 95
85 Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
86 100 105 110
87 Gly Gln Pro Trp Arg Asn Ala Ser Gln Cys Gln Leu Asp Asp Glu Glu
88 115 120 125
89 Ile Glu Val Gln Lys Gly Val Ala Lys Met Tyr Ser Ser Gln Gln Val
90 130 135 140
91 Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala
92 145 150 155 160
93 Leu Val Ile Leu Leu Gly Leu Arg Lys Leu His Cys Thr Arg Asn Tyr
94 165 170 175
95 Ile His Gly Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Gly Ser Val
96 180 185 190
97 Leu Val Ile Asp Trp Leu Leu Lys Thr Arg Tyr Ser Gln Lys Ile Gly
98 195 200 205
99 Asp Asp Leu Ser Val Ser Val Trp Leu Ser Asp Gly Ala Met Ala Gly
100 210 215 220
101 Cys Arg Val Ala Thr Val Ile Met Gln Tyr Gly Ile Ile Pro Asn Tyr
102 225 230 235 240
103 Cys Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Ser Leu Leu Ser Leu
104 245 250 255
105 Ala Thr Phe Ser Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly
106 260 265 270
107 Trp Gly Ala Pro Leu Leu Phe Val Ile Pro Trp Val Val Val Lys Cys
108 275 280 285
109 Leu Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe
110 290 295 300
111 Trp Trp Ile Leu Arg Ile Pro Val Phe Leu Ala Leu Leu Ile Asn Phe

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```

112 305          310          315          320
113 Phe Ile Phe Val His Ile Ile Gln Leu Leu Val Ala Lys Leu Arg Ala
114          325          330          335
115 His Gln Met His Tyr Ala Asp Tyr Lys Phe Arg Leu Ala Arg Ser Thr
116          340          345          350
117 Leu Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe
118          355          360          365
119 Val Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Thr Lys Leu Phe
120          370          375          380
121 Phe Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu
122 385          390          395          400
123 Tyr Cys Phe Leu Asn Lys Glu Val Gln Ala Glu Leu Met Arg Arg Trp
124          405          410          415
125 Arg Gln Trp Gln Glu Gly Lys Ala Leu Gln Glu Glu Arg Leu Ala Ser
126          420          425          430
127 Ser His Gly Ser His Met Ala Pro Ala Gly Pro Cys His Gly Asp Pro
128          435          440          445
129 Cys Glu Lys Leu Gln Leu Met Ser Ala Gly Ser Ser Ser Gly Thr Gly
130          450          455          460
131 Cys Val Pro Ser Met Glu Thr Ser Leu Ala Ser Ser Leu Pro Arg Leu
132 465          470          475          480
133 Ala Asp Ser Pro Thr
134          485
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 200
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Targeting Vector
145 <400> SEQUENCE: 3
146 gcagccgtgg cgcaacgcct cccaatgtca gttggatgat gaagagatcg aggtccaggt 60
147 cagctctgga gggtatgggg tgggtgcaca gcggggctgt gtggggccag gggatacggc 120
148 actgccacgc cccactcggc ctctggtttg cagaaggggg tggccaagat gtatagcagc 180
149 cagcaggtga cgtacaccgt                                     200
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 200
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Targeting Vector
159 <400> SEQUENCE: 4
160 gaggtggtct ttgcctttgt gactgacgag catgcccaag gcaccctgcg ctccaccaag 60
161 ctcttttttg acctgttcct cagctccttc caggtgagtc tccatcatac cccaccctg 120
162 ggaccacagag tgctgtcctt gaccactctc tttctccagg gtctgtctggt ggctgttctc 180
163 tactgtttcc tcaacaagga                                     200
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 2034
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens

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170 <400> SEQUENCE: 5

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171 ggatctggca gcgccgcgaa gacgagcggg caccggcgcc cgacccgagc gcgcccagag 60
172 gacggcgggg agccaagccg acccccagagc agcgccgcgc gggccctgag gctcaaagg 120
173 gcagcttcag gggaggacac cccactggcc aggacgcccc aggtctgct gctctgccac 180
174 tcagctgccc tcggaggagc gtacacacac accaggactg cattgccccca gtgtgcagcc 240
175 cctgccagat gtgggaggca gctagctgcc cagaggcatg cccccctgcc agccacagcg 300
176 acccctgctg ctggttgctg tgctgctggc ctgccagcca caggtcccct ccgctcaggt 360
177 gatggacttc ctgtttgaga agtggaaagt ctacggtgac cagtgtcacc acaacctgag 420
178 cctgctgccc cctcccacgg agctgggtgt caacagaacc ttcgacaagt attcctgctg 480
179 gccggacacc cccgccaata ccacggccaa catctcctgc ccctgggtacc tgccttggca 540
180 ccacaaagtg caacaccgct tcgtgttcaa gagatgcggg cccgacggtc agtgggtgcg 600
181 tggaccccg gggcagcctt ggcgtgatgc ctcccagtg cagatggatg gcgaggagat 660
182 tgagggtccag aaggagggtg ccaagatgta cagcagcttc caggtgatgt acacagtggg 720
183 ctacagcctg tccctggggg ccctgctcct cgccttggcc atcctggggg gcctcagcaa 780
184 gctgcactgc acccgcaatg ccattccacgc gaatctgttt gcgtccttcg tgctgaaagc 840
185 cagctccgtg ctgggtcattg atgggctgct caggaccgcg tacagccaga aaattggcga 900
186 cgacctcagt gtcagcacct ggctcagtga tggagcggg gctggctgcc gtgtggccgc 960
187 ggtgttcatg caatatggca tcgtggccaa ctactgctgg ctgctggtgg agggcctgta 1020
188 cctgcacaac ctgctgggccc tggccaccct ccccgagagg agcttcttca gcctctacct 1080
189 gggcatcggc tgggggtgccc ccattgctgtt cgtcgtcccc tgggcagtgg tcaagtgtct 1140
190 gttcagagaac gtccagtgtt ggaccagcaa tgacaacatg ggcttctggt ggatcctgcg 1200
191 gttccccgtc ttcttgggca tcctgatcaa cttcttcata ttcgtccgca tcgttcagct 1260
192 gctcgtggcc aagctgcggg cacggcagat gcaccacaca gactacaagt tccggctggc 1320
193 caagtccacg ctgaccctca tccctctgct gggcgtccac gaagtggctt ttgccttcgt 1380
194 gacggacgag cacgcccagg gcaccctgcg ctccgccaag ctcttcttcg acctcttcct 1440
195 cagctccttc cagggcctgc tgggtgctgt cctctactgc ttctcaaca aggaggtgca 1500
196 gtcggagctg cggcggcgtt ggcaccgtg gcgcctggg aaagtgtat gggaggagcg 1560
197 gaacaccagc aaccacagg cctcatcttc gcccggccac ggccctccca gcaaggagct 1620
198 gcagtttggg aggggtggtg gcagccagga ttcatctgcg gagacccctc tggctggtgg 1680
199 cctccctaga ttggctgaga gcccctctg aacctgctg ggaccccagc tagggctgga 1740
200 ctctggcacc cagaggcgtc gctggacaac ccagaactgg acgcccagct gaggtgagg 1800
201 gcgggggagc caacagcagc cccacacct ccccccaccc cagtgtggct gtctgcgaga 1860
202 ttgggcctcc tctccctgca cctgccttgt cctggtgca gaggtgagca gaggagtcca 1920
203 gggcgggagt gggggctgtg ccgtgaactg cgtgccagtg tccccacgta tgtcggcacg 1980
204 tcccatgtgc atggaaatgt cctccaacaa taaagagctc aagtggtcac cgtg 2034

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206 <210> SEQ ID NO: 6

207 <211> LENGTH: 477

208 <212> TYPE: PRT

209 <213> ORGANISM: Homo sapiens

211 <400> SEQUENCE: 6

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212 Met Pro Pro Cys Gln Pro Gln Arg Pro Leu Leu Leu Leu Leu Leu
213 1 5 10 15
214 Leu Ala Cys Gln Pro Gln Val Pro Ser Ala Gln Val Met Asp Phe Leu
215 20 25 30
216 Phe Glu Lys Trp Lys Leu Tyr Gly Asp Gln Cys His His Asn Leu Ser
217 35 40 45
218 Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp Lys
219 50 55 60
220 Tyr Ser Cys Trp Pro Asp Thr Pro Ala Asn Thr Thr Ala Asn Ile Ser

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221	65					70					75					80
222	Cys	Pro	Trp	Tyr	Leu	Pro	Trp	His	His	Lys	Val	Gln	His	Arg	Phe	Val
223					85					90					95	
224	Phe	Lys	Arg	Cys	Gly	Pro	Asp	Gly	Gln	Trp	Val	Arg	Gly	Pro	Arg	Gly
225				100					105					110		
226	Gln	Pro	Trp	Arg	Asp	Ala	Ser	Gln	Cys	Gln	Met	Asp	Gly	Glu	Glu	Ile
227			115					120					125			
228	Glu	Val	Gln	Lys	Glu	Val	Ala	Lys	Met	Tyr	Ser	Ser	Phe	Gln	Val	Met
229		130					135					140				
230	Tyr	Thr	Val	Gly	Tyr	Ser	Leu	Ser	Leu	Gly	Ala	Leu	Leu	Leu	Ala	Leu
231	145					150					155					160
232	Ala	Ile	Leu	Gly	Gly	Leu	Ser	Lys	Leu	His	Cys	Thr	Arg	Asn	Ala	Ile
233					165					170					175	
234	His	Ala	Asn	Leu	Phe	Ala	Ser	Phe	Val	Leu	Lys	Ala	Ser	Ser	Val	Leu
235				180					185					190		
236	Val	Ile	Asp	Gly	Leu	Leu	Arg	Thr	Arg	Tyr	Ser	Gln	Lys	Ile	Gly	Asp
237			195					200					205			
238	Asp	Leu	Ser	Val	Ser	Thr	Trp	Leu	Ser	Asp	Gly	Ala	Val	Ala	Gly	Cys
239		210					215					220				
240	Arg	Val	Ala	Ala	Val	Phe	Met	Gln	Tyr	Gly	Ile	Val	Ala	Asn	Tyr	Cys
241	225					230					235					240
242	Trp	Leu	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu	Leu	Gly	Leu	Ala
243				245						250					255	
244	Thr	Leu	Pro	Glu	Arg	Ser	Phe	Phe	Ser	Leu	Tyr	Leu	Gly	Ile	Gly	Trp
245			260						265					270		
246	Gly	Ala	Pro	Met	Leu	Phe	Val	Val	Pro	Trp	Ala	Val	Val	Lys	Cys	Leu
247		275						280					285			
248	Phe	Glu	Asn	Val	Gln	Cys	Trp	Thr	Ser	Asn	Asp	Asn	Met	Gly	Phe	Trp
249		290					295					300				
250	Trp	Ile	Leu	Arg	Phe	Pro	Val	Phe	Leu	Ala	Ile	Leu	Ile	Asn	Phe	Phe
251	305					310					315					320
252	Ile	Phe	Val	Arg	Ile	Val	Gln	Leu	Leu	Val	Ala	Lys	Leu	Arg	Ala	Arg
253				325						330					335	
254	Gln	Met	His	His	Thr	Asp	Tyr	Lys	Phe	Arg	Leu	Ala	Lys	Ser	Thr	Leu
255			340						345					350		
256	Thr	Leu	Ile	Pro	Leu	Leu	Gly	Val	His	Glu	Val	Val	Phe	Ala	Phe	Val
257		355						360					365			
258	Thr	Asp	Glu	His	Ala	Gln	Gly	Thr	Leu	Arg	Ser	Ala	Lys	Leu	Phe	Phe
259		370					375					380				
260	Asp	Leu	Phe	Leu	Ser	Ser	Phe	Gln	Gly	Leu	Leu	Val	Ala	Val	Leu	Tyr
261	385					390					395					400
262	Cys	Phe	Leu	Asn	Lys	Glu	Val	Gln	Ser	Glu	Leu	Arg	Arg	Arg	Trp	His
263				405						410					415	
264	Arg	Trp	Arg	Leu	Gly	Lys	Val	Leu	Trp	Glu	Glu	Arg	Asn	Thr	Ser	Asn
265			420						425					430		
266	His	Arg	Ala	Ser	Ser	Ser	Pro	Gly	His	Gly	Pro	Pro	Ser	Lys	Glu	Leu
267		435						440					445			
268	Gln	Phe	Gly	Arg	Gly	Gly	Gly	Ser	Gln	Asp	Ser	Ser	Ala	Glu	Thr	Pro
269		450					455					460				

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date